SCORE Search Results Details for Application 10529592 and Search Result 20080410_005516_us-10-529-592a-2.rag.

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This page gives you Search Results detail for the Application 10529592 and Search Result 20080410_005516_us-10-529-592a-2.rag.

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GenCore version 6.2.1

OM protein - protein search, using sw model

Run on: April 10, 2008, 01:12:17 ; Search time 310 Seconds
(without alignments)
147.399 Million cell updates/sec

Title: US-10-529-592A-2
Perfect score: 411
Sequence: 1 MGLKMSCLKGFQMCVSSSSS.....TVWLDETGSCPDDGEIDPEA 76

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3405708 seqs, 601879884 residues

Total number of hits satisfying chosen parameters: 3405708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200711:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000:*
4: geneseqp2001:*
5: geneseqp2002:*
6: geneseqp2003a:*
7: geneseqp2003b:*
8: geneseqp2004a:*

9: geneseqp2004b:*
10: geneseqp2005:*
11: geneseqp2006:*
12: geneseqp2007:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	411	100.0	76	8	ADM96968	Adm96968 Human pan
2	411	100.0	76	12	AES72472	Aes72472 Human C19
3	401	97.6	76	12	AES72498	Aes72498 Human C19
4	365	88.8	538	7	ADE08404	Ade08404 Novel pro
5	229.5	55.8	82	4	AAM92673	Aam92673 Human dig
6	88	21.4	30	12	AES72478	Aes72478 C1958-PP3
7	78.5	19.1	278	8	AFP64650	Afp64650 Glycine m
8	78.5	19.1	467	11	AFC46406	Afc46406 Soybean a
9	78.5	19.1	469	11	AFC46405	Afc46405 Soybean a
10	78	19.0	16	12	AES72496	Aes72496 Human C19
11	78	19.0	30	12	AES72479	Aes72479 C1958-PP3
12	73	17.8	3792	11	AEJ38171	Aej38171 P. cellul
13	72.5	17.6	510	5	AAO17533	Aao17533 B glumae
14	72	17.5	96	8	AFP89144	Afp89144 Glycine m
15	70.5	17.2	1302	6	ABU18188	Abu18188 Protein e
16	70	17.0	338	8	ADT59586	Adt59586 Plant pol
17	68.5	16.7	321	9	AFP80209	Afp80209 Glycine m
18	68.5	16.7	332	10	ADY30823	Ady30823 Thale cre
19	68.5	16.7	495	8	ADN18160	Adn18160 Bacterial
20	68.5	16.7	611	5	AAU78365	Aau78365 Arabidops
21	68.5	16.7	611	10	ADY30825	Ady30825 Thale cre
22	68	16.5	174	9	AFP54677	Afp54677 Glycine m
23	68	16.5	298	2	AAW19008	Aaw19008 Feline he
24	68	16.5	389	8	ADT58785	Adt58785 Plant pol
25	67	16.3	227	11	AEF73243	Aef73243 Rat deriv
26	67	16.3	389	8	ADJ34689	Adj34689 Cow 2'-5'
27	67	16.3	396	11	AEF73238	Aef73238 Rat deriv
28	67	16.3	544	2	AAW28866	Aaw28866 Rat brain
29	67	16.3	544	3	AAY87746	Aay87746 Rat brain
30	67	16.3	544	6	ADD46213	Add46213 Rat Prote
31	67	16.3	544	6	ADE62455	Ade62455 Rat Prote
32	67	16.3	544	6	ADE62451	Ade62451 Rat Prote
33	67	16.3	544	11	AEF73245	Aef73245 Rat neuro
34	66.5	16.2	84	3	AAB12328	Aab12328 Human sec
35	66.5	16.2	112	3	AAB12364	Aab12364 Fragment

36	66.5	16.2	384	8	ADU02510	Adu02510 Novel hum
37	66.5	16.2	395	8	ADX90093	Adx90093 Plant ful
38	66	16.1	2220	8	ADJ48798	Adj48798 Oil-assoc
39	65.5	15.9	439	7	ADD14956	Add14956 Human UP
40	65.5	15.9	439	8	ADI13452	Adi13452 Human UPH
41	65.5	15.9	439	8	ADQ67957	Adq67957 Human hep
42	65.5	15.9	537	10	AEN24565	Aen24565 Cucumis m
43	65.5	15.9	622	5	AAU93158	Aau93158 Arabidops
44	65.5	15.9	622	12	AER67985	Aer67985 Diabetes
45	65.5	15.9	933	11	AEH82012	Aeh82012 Microbulb

ALIGNMENTS

RESULT 1
ADM96968
ID ADM96968 standard; protein; 76 AA.
XX
AC ADM96968;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human pancreatic cancer upregulated protein C1958V1.
XX
KW cytostatic; gene therapy; pancreatic cancer; diagnosis;
KW anti-tumor immunity.
XX
OS Homo sapiens.
XX
PN WO2004031411-A2.
XX
PD 15-APR-2004.
XX
PF 12-SEP-2003; 2003WO-JP011713.
XX
PR 30-SEP-2002; 2002US-0414872P.
PR 28-FEB-2003; 2003US-0450889P.
XX
PA (ONCO-) ONCOTHERAPY SCI INC.
PA (UYTY) UNIV TOKYO.
XX
PI Nakamura Y, Katagiri T;
XX
DR WPI; 2004-330204/30.
DR N-PSDB; ADM96967.
XX
PT New C1958V1 or C1958V2 polypeptides, useful in useful in diagnosing and
PT treating pancreatic cancer and in inducing anti tumor immunity.

XX
PS Claim 1; SEQ ID NO 2; 71pp; English.
XX
CC The invention relates to the isolation of novel genes upregulated in
CC pancreatic cancer designated C1958V1 and C1958V2, their encoded
CC polypeptides (I), a sequence in which one or more amino acids are
CC substituted, deleted, inserted, and/or added and that has a biological
CC activity equivalent to the C1958V1 or C1958V2 proteins; or a sequence
CC encoded by a polynucleotide that hybridizes under stringent conditions to
CC the C1958V1 or C1958V2 polynucleotides. The polypeptides and
CC polynucleotides, compounds and compositions are useful in diagnosing and
CC treating pancreatic cancer and in inducing anti tumor immunity. This
CC sequence represents the C1958V1 protein sequence.
XX
SQ Sequence 76 AA;

Query Match 100.0%; Score 411; DB 8; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MGLKMSCLKGFQMCVSSSSSSHDEAPVLNDKHLDVPDIIITPPTPTGMMLPRDLGSTVWL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGLKMSCLKGFQMCVSSSSSSHDEAPVLNDKHLDVPDIIITPPTPTGMMLPRDLGSTVWL 60

Qy         61 DETGSCPDDGEIDPEA 76
              ||||||||||||||||
Db         61 DETGSCPDDGEIDPEA 76
```

RESULT 2
AES72472
ID AES72472 standard; protein; 76 AA.
XX
AC AES72472;
XX
DT 03-MAY-2007 (first entry)
XX
DE Human C1958 splice variant 1, protein.
XX
KW Pancreatic ductal adenocarcinoma; cancer; cytostatic; tumor marker;
KW protein therapy; screening; splice variant; C1958V1; apoptosis;
KW gene therapy; pancreas tumor; lung tumor; renal tumor; testicle tumor.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Binding-site 36. .41
FT /note= "PPP3CA binding site, specifcally claimed in claim
FT 29"

XX
PN WO2007013358-A2.
XX
PD 01-FEB-2007.
XX
PF 14-JUL-2006; 2006WO-JP314442.
XX
PR 28-JUL-2005; 2005US-0703791P.
XX
PA (ONCO-) ONCOTHERAPY SCI INC.
PA (UYTY) UNIV TOKYO.
XX
PI Nakamura Y, Katagiri T, Inaki K;
XX
DR WPI; 2007-283242/27.
DR N-PSDB; AES72471.
XX
PT New VIVIT polypeptide useful for treating or preventing cancer, such as
PT pancreatic cancer, lung cancer, kidney cancer and testicular tumor.
XX
PS Disclosure; SEQ ID NO 2; 78pp; English.
XX
CC The invention relates to a VIVIT polypeptide (AES72497) and at least a
CC fragment of the human C1958 sequence appearing as AES72472, in which
CC residues at positions 37-41 is replaced with AES72497, or an amino acid
CC sequence of a polypeptide functionally equivalent to the polypeptide
CC comprising the fragment sequence. Also included are an agent for
CC treating/preventing cancer (comprising as an active ingredient the VIVIT
CC polypeptide, or a polynucleotide encoding the polypeptide), a
CC pharmaceutical composition (comprising the VIVIT polypeptide, and a
CC carrier), screening (M1) for a compound useful in treating/preventing
CC cancers (involving (a) contacting a polypeptide comprising a PPP3CA-
CC binding domain of a C1958 polypeptide with a polypeptide comprising a
CC C1958-binding domain of a PPP3CA polypeptide in the presence of a test
CC compound, (b) detecting binding between the polypeptides, and (c)
CC selecting a test compound that inhibits binding between the
CC polypeptides), a kit for screening for a compound for treating or
CC preventing cancers, treating/preventing cancers in a subject (involving
CC administering the compound selected above), and inducing apoptosis in a
CC cell (involving introducing a polypeptide having a dominant-negative
CC effect against C1958 or a polynucleotide encoding the polypeptide into
CC the cell, where the polypeptide comprises a fragment sequence having
CC AES72497, or the mutated C1958 above). The polypeptide is modified with a
CC cell-membrane permeable substance, which has the general formula [R]-[D],
CC where [R] represents the cell-membrane permeable substance, and [D]
CC represents the amino acid sequence of a fragment sequence of AES72497, or
CC the mutated C1958 peptide. The VIVIT polypeptide is useful for treating
CC and/or preventing cancer, preferably pancreatic cancer (especially
CC Pancreatic ductal adenocarcinoma), lung cancer, kidney cancer and

```
CC   testicular tumor. (M1) is useful for screening a compound for treating or
CC   preventing cancers. The present sequence represents a splice variant
CC   protein of human C1958.
XX
SQ   Sequence 76 AA;

  Query Match             100.0%;  Score 411;  DB 12;  Length 76;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-44;
  Matches   76;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGLKMSCLKGFQMCVSSSSSSHDEAPVLNDKHLDVPDIIITPPTPTGMMLPRDLGSTVWL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGLKMSCLKGFQMCVSSSSSSHDEAPVLNDKHLDVPDIIITPPTPTGMMLPRDLGSTVWL 60

Qy         61 DETGSCPDDGEIDPEA 76
              ||||||||||||||||
Db         61 DETGSCPDDGEIDPEA 76


RESULT 3
AES72498
ID   AES72498 standard; protein; 76 AA.
XX
AC   AES72498;
XX
DT   03-MAY-2007  (first entry)
XX
DE   Human C1958 protein mutant.
XX
KW   Pancreatic ductal adenocarcinoma; cancer; cytostatic; tumor marker;
KW   protein therapy; screening; mutein; C1958V1; apoptosis; gene therapy;
KW   pancreas tumor; lung tumor; renal tumor; testicle tumor.
XX
OS   Homo sapiens.
OS   Synthetic.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 37. .41
FT                   /note= "Wild-type Asp-Ile-Ile-ILe-Thr has been
FT                   substituted by Val-Ile-Val-Ile-Thr"
XX
PN   WO2007013358-A2.
XX
PD   01-FEB-2007.
XX
PF   14-JUL-2006; 2006WO-JP314442.
XX
PR   28-JUL-2005; 2005US-0703791P.
```

XX
PA (ONCO-) ONCOTHERAPY SCI INC.
PA (UYTY) UNIV TOKYO.
XX
PI Nakamura Y, Katagiri T, Inaki K;
XX
DR WPI; 2007-283242/27.
XX
PT New VIVIT polypeptide useful for treating or preventing cancer, such as
PT pancreatic cancer, lung cancer, kidney cancer and testicular tumor.
XX
PS Claim 1; Page; 78pp; English.
XX
CC The invention relates to a VIVIT polypeptide (AES72497) and at least a
CC fragment of the human C1958 sequence appearing as AES72472, in which
CC residues at positions 37-41 is replaced with AES72497, or an amino acid
CC sequence of a polypeptide functionally equivalent to the polypeptide
CC comprising the fragment sequence. Also included are an agent for
CC treating/preventing cancer (comprising as an active ingredient the VIVIT
CC polypeptide, or a polynucleotide encoding the polypeptide), a
CC pharmaceutical composition (comprising the VIVIT polypeptide, and a
CC carrier), screening (M1) for a compound useful in treating/preventing
CC cancers (involving (a) contacting a polypeptide comprising a PPP3CA-
CC binding domain of a C1958 polypeptide with a polypeptide comprising a
CC C1958-binding domain of a PPP3CA polypeptide in the presence of a test
CC compound, (b) detecting binding between the polypeptides, and (c)
CC selecting a test compound that inhibits binding between the
CC polypeptides), a kit for screening for a compound for treating or
CC preventing cancers, treating/preventing cancers in a subject (involving
CC administering the compound selected above), and inducing apoptosis in a
CC cell (involving introducing a polypeptide having a dominant-negative
CC effect against C1958 or a polynucleotide encoding the polypeptide into
CC the cell, where the polypeptide comprises a fragment sequence having
CC AES72497, or the mutated C1958 above). The polypeptide is modified with a
CC cell-membrane permeable substance, which has the general formula [R]-[D],
CC where [R] represents the cell-membrane permeable substance, and [D]
CC represents the amino acid sequence of a fragment sequence of AES72497, or
CC the mutated C1958 peptide. The VIVIT polypeptide is useful for treating
CC and/or preventing cancer, preferably pancreatic cancer (especially
CC Pancreatic ductal adenocarcinoma), lung cancer, kidney cancer and
CC testicular tumor. (M1) is useful for screening a compound for treating or
CC preventing cancers. The present sequence represents a mutant of human
CC C1958V1, where the PPP3CA binding site at 37-41 has been replaced by the
CC VIVIT peptide. NOTE: The present sequence is not shown in the
CC specification but was created by the indexer using the information in the
CC claims and the wild-type C1958V1 sequence.
XX
SQ Sequence 76 AA;

```
  Query Match             97.6%;  Score 401;  DB 12;  Length 76;
  Best Local Similarity   97.4%;  Pred. No. 2.5e-43;
  Matches   74;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MGLKMSCLKGFQMCVSSSSSSHDEAPVLNDKHLDVPDIIITPPTPTGMMLPRDLGSTVWL 60
              |||||||||||||||||||||||||||||||| |:||||||||||||||||||||
Db          1 MGLKMSCLKGFQMCVSSSSSSHDEAPVLNDKHLDVPVIVITPPTPTGMMLPRDLGSTVWL 60

Qy         61 DETGSCPDDGEIDPEA 76
              ||||||||||||||||
Db         61 DETGSCPDDGEIDPEA 76


RESULT 4
ADE08404
ID   ADE08404 standard; protein; 538 AA.
XX
AC   ADE08404;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Novel protein (useful for identifying genetic disorders) #559.
XX
KW   novel gene; novel protein; tissue marker; molecular weight marker;
KW   chromosome marker; genetic disorder.
XX
OS   Unidentified.
XX
PN   WO2003054152-A2.
XX
PD   03-JUL-2003.
XX
PF   10-DEC-2002; 2002WO-US039555.
XX
PR   10-DEC-2001; 2001US-0339739P.
PR   11-DEC-2001; 2001US-0339453P.
PR   14-MAR-2002; 2002US-0365091P.
PR   14-MAR-2002; 2002US-0365384P.
PR   12-APR-2002; 2002US-0372381P.
PR   12-APR-2002; 2002US-0372615P.
PR   22-APR-2002; 2002US-00128558.
PR   24-APR-2002; 2002US-0376045P.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Asundi V,  Goodrich RW,  Ren F,  Zhang J,  Zhao QA,  Wang J;
PI   Ghosh M,  Xue AJ,  Wehrman T,  Weng G,  Zhou P,  Drmanac RT,  Wang Z;
PI   Ma Y,  Wang D,  Chen R,  Xu C,  Boyle BJ;
XX
```

DR   WPI; 2003-569235/53.
DR   N-PSDB; ADE07493.
XX
PT   New polynucleotides, useful for expressing recombinant proteins for
PT   analysis, characterization or therapeutic use, or as markers for tissues
PT   in which the corresponding protein is preferentially expressed.
XX
PS   Claim 20; SEQ ID NO 1470; 1177pp; English.
XX
CC   The invention comprises the amino acid and coding sequences of novel
CC   proteins. The DNA and protein sequences of the invention are useful as:
CC   markers for tissues in which the corresponding protein is preferentially
CC   expressed; as molecular weight markers on gels; as chromosome markers or
CC   tags; to identify chromosomes or to map related gene positions; and to
CC   compare with endogenous DNA sequences in patients to identify potential
CC   genetic disorders. The present amino acid sequence represents a protein
CC   of the invention.
XX
SQ   Sequence 538 AA;

  Query Match   88.8%; Score 365; DB 7; Length 538;
  Best Local Similarity   98.5%; Pred. No. 1.2e-37;
  Matches   67; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   9 KGFQMCVSSSSSSHDEAPVLNDKHLDVPDIIITPPTPTGMMLPRDLGSTVWLDETGSCPD 68
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   471 QGFQMCVSSSSSSHDEAPVLNDKHLDVPDIIITPPTPTGMMLPRDLGSTVWLDETGSCPD 530

Qy   69 DGEIDPEA 76
              ||||||||
Db   531 DGEIDPEA 538

RESULT 5
AAM92673
ID   AAM92673 standard; protein; 82 AA.
XX
AC   AAM92673;
XX
DT   06-NOV-2001 (first entry)
XX
DE   Human digestive system antigen SEQ ID NO: 2022.
XX
KW   Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW   ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW   digestive system disorder; Meckel's diverticulum.
XX
OS   Homo sapiens.
XX

PN WO200155314-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001324.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
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PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.

PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
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PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
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PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
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PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
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PR 20-OCT-2000; 2000US-0241787P.
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PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
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PR 08-NOV-2000; 2000US-0246477P.

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PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
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PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
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PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX

DR WPI; 2001-502630/55.
DR N-PSDB; AAK88446.
XX
PT Polynucleotides encoding digestive system antigens, useful for
PT diagnosing, treating, preventing and/or prognozing disorders of the
PT digestive system, particularly cancer and cancer metastases.
XX
PS Claim 11; SEQ ID NO 2022; 986pp; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human digestive system antigens. These can be used in the
CC diagnosis, treatment and prevention of digestive system disorders,
CC including cancer, Meckel's diverticulum, bacterial or parasitic
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC ulcerative colitis. The present sequence is a digestive system antigen of
CC the invention
XX
SQ Sequence 82 AA;

Query Match 55.8%; Score 229.5; DB 4; Length 82;
Best Local Similarity 59.0%; Pred. No. 3.2e-21;
Matches 49; Conservative 7; Mismatches 12; Indels 15; Gaps 3;

```
Qy          1 MGLKMSCLKGFQMCVSSSSSS-------HDEAPVLNDKHLDVPDIIITPPTPTGMMLPRD 53
              ||||||||| |: |||:::::         :||     |   |        |||||||||
Db          8 MGLKMSCLKAFK-CVSAAAAAATTRPRPEXQAPGRARHHHHAPH-------PTGMMLPRD 59

Qy         54 LGSTVWLDETGSCPDDGEIDPEA 76
              ||||||||||||||||||||||
Db         60 LGSTVWLDETGSCPDDGEIDPEA 82
```

RESULT 6
AES72478
ID AES72478 standard; peptide; 30 AA.
XX
AC AES72478;
XX
DT 03-MAY-2007 (first entry)
XX
DE C1958-PP3CA inhibitory peptide SEQ ID NO:8.
XX
KW Pancreatic ductal adenocarcinoma; cancer; cytostatic; tumor marker;
KW protein therapy; screening; apoptosis; gene therapy; pancreas tumor;
KW lung tumor; renal tumor; testicle tumor; C1958.
XX
OS Homo sapiens.
OS Synthetic.
XX

PN WO2007013358-A2.
XX
PD 01-FEB-2007.
XX
PF 14-JUL-2006; 2006WO-JP314442.
XX
PR 28-JUL-2005; 2005US-0703791P.
XX
PA (ONCO-) ONCOTHERAPY SCI INC.
PA (UYTY) UNIV TOKYO.
XX
PI Nakamura Y, Katagiri T, Inaki K;
XX
DR WPI; 2007-283242/27.
XX
PT New VIVIT polypeptide useful for treating or preventing cancer, such as
PT pancreatic cancer, lung cancer, kidney cancer and testicular tumor.
XX
PS Example; SEQ ID NO 8; 78pp; English.
XX
CC The invention relates to a VIVIT polypeptide (AES72497) and at least a
CC fragment of the human C1958 sequence appearing as AES72472, in which
CC residues at positions 37-41 is replaced with AES72497, or an amino acid
CC sequence of a polypeptide functionally equivalent to the polypeptide
CC comprising the fragment sequence. Also included are an agent for
CC treating/preventing cancer (comprising as an active ingredient the VIVIT
CC polypeptide, or a polynucleotide encoding the polypeptide), a
CC pharmaceutical composition (comprising the VIVIT polypeptide, and a
CC carrier), screening (M1) for a compound useful in treating/preventing
CC cancers (involving (a) contacting a polypeptide comprising a PPP3CA-
CC binding domain of a C1958 polypeptide with a polypeptide comprising a
CC C1958-binding domain of a PPP3CA polypeptide in the presence of a test
CC compound, (b) detecting binding between the polypeptides, and (c)
CC selecting a test compound that inhibits binding between the
CC polypeptides), a kit for screening for a compound for treating or
CC preventing cancers, treating/preventing cancers in a subject (involving
CC administering the compound selected above), and inducing apoptosis in a
CC cell (involving introducing a polypeptide having a dominant-negative
CC effect against C1958 or a polynucleotide encoding the polypeptide into
CC the cell, where the polypeptide comprises a fragment sequence having
CC AES72497, or the mutated C1958 above). The polypeptide is modified with a
CC cell-membrane permeable substance, which has the general formula [R]-[D],
CC where [R] represents the cell-membrane permeable substance, and [D]
CC represents the amino acid sequence of a fragment sequence of AES72497, or
CC the mutated C1958 peptide. The VIVIT polypeptide is useful for treating
CC and/or preventing cancer, preferably pancreatic cancer (especially
CC Pancreatic ductal adenocarcinoma), lung cancer, kidney cancer and
CC testicular tumor. (M1) is useful for screening a compound for treating or
CC preventing cancers. The present sequence is a C1958 test peptide

```
CC   comprising a polyArginine cell permeable peptide linked via a linker
CC   peptide to a C1958 peptide.
XX
SQ   Sequence 30 AA;

  Query Match             21.4%;  Score 88;  DB 12;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0.0015;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 KHLDVPDIIITPPTPT 46
              ||||||||||||||||
Db         15 KHLDVPDIIITPPTPT 30


RESULT 7
AFP64650
ID   AFP64650 standard; protein; 278 AA.
XX
AC   AFP64650;
XX
DT   18-OCT-2007  (first entry)
XX
DE   Glycine max protein SEQ ID NO:155828.
XX
KW   plant; cold tolerance; heat tolerance; drought resistance;
KW   herbicide resistance; pathogen resistance; pesticide resistance;
KW   disease-resistance; crop improvement; insect resistance;
KW   nitrogen fixation; plant growth regulation; plant disease;
KW   stress tolerance; seed oil; transgenic.
XX
OS   Glycine max.
XX
PN   US2004031072-A1.
XX
PD   12-FEB-2004.
XX
PF   28-APR-2003; 2003US-00424599.
XX
PR   06-MAY-1999;   99US-00304517.
PR   05-NOV-2001; 2001US-00985678.
XX
PA   (LROS/) LA ROSA T J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (CAOY/) CAO Y.
XX
PI   La Rosa TJ,  Zhou Y,  Kovalic DK,  Cao Y;
XX
DR   WPI; 2004-168999/16.
```

XX
PT New recombinant DNA construct, useful in producing plants with desired
PT properties, e.g. increased cold, heat or drought tolerance or tolerance
PT to herbicides, extreme osmotic conditions or pathogens and improved plant
PT growth and development.
XX
PS Claim 2; SEQ ID NO 155828; 15pp; English.
XX
CC The invention relates to a recombinant DNA construct, polynucleotides or
CC polypeptides which are useful in improving plant cold, heat or drought
CC tolerance or tolerance to herbicides, extreme osmotic conditions,
CC pathogens or pests, in improving yield by modification of photosynthesis
CC or of carbohydrate, nitrogen or phosphorus use and/or uptake, in
CC manipulating growth rate in plant cells by modification of the cell cycle
CC pathway, in providing increased resistance to plant disease and improved
CC plant growth and development under at least one stress condition, in
CC producing galactomannan, plant growth regulators and lignin, in
CC increasing the rate of homologous recombination in plants, in modifying
CC seed oil yield and/or content and seed protein yield and/or content and
CC in encoding a plant transcription factor. The present sequence represents
CC a Glycine max protein of the invention. Note: This sequence is not shown
CC in the specification but was obtained in electronic format directly from
CC USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 278 AA;

Query Match 19.1%; Score 78.5; DB 8; Length 278;
Best Local Similarity 37.3%; Pred. No. 0.41;
Matches 25; Conservative 8; Mismatches 23; Indels 11; Gaps 5;

```
Qy         12 QMCVSSSSSSHDEAPVLNDK-HLDVPD---IIITPPTPTGMMLPRDLGSTVWLDETGSCP 67
              |  :    :||   |:|  | |||  :     :||||||  : | || ||  : :   |
Db         55 QNALHKLQNSH---PILRSKIHLDPSNNTFHFLTPPTPTVQIHPFDLASTAHIIQ---CQ 108

Qy         68 DDGEIDP 74
               ||  ||
Db        109 SDGH-DP 114
```

RESULT 8
AFC46406
ID AFC46406 standard; protein; 467 AA.
XX
AC AFC46406;
XX
DT 20-SEP-2007 (first entry)
XX
DE Soybean amino acid sequence SEQ ID NO 7776.
XX

KW plant; DNA mapping; gene expression.
XX
OS Glycine max.
XX
PN US2006048240-A1.
XX
PD 02-MAR-2006.
XX
PF 01-APR-2005; 2005US-00096568.
XX
PR 01-APR-2004; 2004US-0558095P.
XX
PA (ALEX/) ALEXANDROV N.
PA (BROV/) BROVER V.
XX
PI Alexandrov N, Brover V;
XX
DR WPI; 2006-421739/43.
XX
PT New isolated Sequence-Determined DNA Fragments (SDFs) from different
PT plant species, e.g. corn, wheat, soybean, or rice, useful for controlling
PT behavior of a gene in the chromosome or identifying a particular
PT individual organism.
XX
PS Claim 9; SEQ ID NO 7776; 87pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule from the
CC genome of a plant. Also described: (1) a vector construct comprising: (a)
CC a first nucleic acid having a regulatory sequence capable of causing
CC transcription and/or translation; and (b) a second nucleic acid having
CC the sequence of the isolated nucleic acid molecule above, where the first
CC and second nucleic acids are operably linked, and where the second
CC nucleic acid is heterologous to any element in the vector construct; (2)
CC a host cell comprising the isolated nucleic acid molecule above, where
CC the nucleic acid molecule is flanked by an exogenous sequence, or
CC comprising the vector construct above; (3) an isolated polypeptide
CC comprising an amino acid sequence: (a) exhibiting at least 40-90%
CC sequence identity of an amino acid sequence encoded by a sequence given
CC in the specification or the Sequence Listing, or its fragment; and (b)
CC capable of exhibiting at least one of the biological activities of the
CC polypeptide encoded by the nucleotide sequence in (a); (4) an antibody
CC capable of binding the isolated polypeptide; (5) introducing an isolated
CC nucleic acid into a host cell; (6) transforming a host cell; (7)
CC modulating transcription and/or translation of the nucleic acid in a host
CC cell; (8) detecting a nucleic acid in a sample; (9) a plant or cell of a
CC plant comprising the nucleic acid molecule, which is exogenous or
CC heterologous to the plant or plant cell, or comprising the vector
CC construct above; and (10) a plant regenerated from the plant cell above.
CC The nucleic acids are useful for specifying a gene product in cells,

```
CC   either as a promoter or as a protein coding sequence or as an UTR or as a
CC   3' termination sequence. They are also useful in controlling the behavior
CC   of a gene in the chromosome, controlling the expression of a gene or as
CC   tools for genetic mapping, recognizing or isolating identical or related
CC   DNA fragments, or identifying a particular individual organism, or
CC   clustering of a group of organisms with a common trait. The present
CC   sequence represents a specifically claimed soybean amino acid sequence
CC   from the present invention. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in
CC   electronic format directly from the USPTO web site.
XX
SQ   Sequence 467 AA;

  Query Match             19.1%;  Score 78.5;  DB 11;  Length 467;
  Best Local Similarity   37.3%;  Pred. No. 0.78;
  Matches   25;  Conservative    8;  Mismatches   23;  Indels   11;  Gaps    5;

Qy         12 QMCVSSSSSSHDEAPVLNDK-HLDVPD---IIITPPTPTGMMLPRDLGSTVWLDETGSCP 67
              |  :    :||   |:|  | |||  :     :||||||  : | || ||  : :   |
Db         54 QNALHKLQNSH---PILRSKIHLDPSNNTFHFLTPPTPTVQIHPFDLASTAHIIQ---CQ 107

Qy         68 DDGEIDP 74
               ||  ||
Db        108 SDGH-DP 113


RESULT 9
AFC46405
ID   AFC46405 standard; protein; 469 AA.
XX
AC   AFC46405;
XX
DT   20-SEP-2007  (first entry)
XX
DE   Soybean amino acid sequence SEQ ID NO 7775.
XX
KW   plant; DNA mapping; gene expression.
XX
OS   Glycine max.
XX
PN   US2006048240-A1.
XX
PD   02-MAR-2006.
XX
PF   01-APR-2005; 2005US-00096568.
XX
PR   01-APR-2004; 2004US-0558095P.
XX
PA   (ALEX/) ALEXANDROV N.
```

PA (BROV/) BROVER V.
XX
PI Alexandrov N, Brover V;
XX
DR WPI; 2006-421739/43.
XX
PT New isolated Sequence-Determined DNA Fragments (SDFs) from different
PT plant species, e.g. corn, wheat, soybean, or rice, useful for controlling
PT behavior of a gene in the chromosome or identifying a particular
PT individual organism.
XX
PS Claim 9; SEQ ID NO 7775; 87pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule from the
CC genome of a plant. Also described: (1) a vector construct comprising: (a)
CC a first nucleic acid having a regulatory sequence capable of causing
CC transcription and/or translation; and (b) a second nucleic acid having
CC the sequence of the isolated nucleic acid molecule above, where the first
CC and second nucleic acids are operably linked, and where the second
CC nucleic acid is heterologous to any element in the vector construct; (2)
CC a host cell comprising the isolated nucleic acid molecule above, where
CC the nucleic acid molecule is flanked by an exogenous sequence, or
CC comprising the vector construct above; (3) an isolated polypeptide
CC comprising an amino acid sequence: (a) exhibiting at least 40-90%
CC sequence identity of an amino acid sequence encoded by a sequence given
CC in the specification or the Sequence Listing, or its fragment; and (b)
CC capable of exhibiting at least one of the biological activities of the
CC polypeptide encoded by the nucleotide sequence in (a); (4) an antibody
CC capable of binding the isolated polypeptide; (5) introducing an isolated
CC nucleic acid into a host cell; (6) transforming a host cell; (7)
CC modulating transcription and/or translation of the nucleic acid in a host
CC cell; (8) detecting a nucleic acid in a sample; (9) a plant or cell of a
CC plant comprising the nucleic acid molecule, which is exogenous or
CC heterologous to the plant or plant cell, or comprising the vector
CC construct above; and (10) a plant regenerated from the plant cell above.
CC The nucleic acids are useful for specifying a gene product in cells,
CC either as a promoter or as a protein coding sequence or as an UTR or as a
CC 3' termination sequence. They are also useful in controlling the behavior
CC of a gene in the chromosome, controlling the expression of a gene or as
CC tools for genetic mapping, recognizing or isolating identical or related
CC DNA fragments, or identifying a particular individual organism, or
CC clustering of a group of organisms with a common trait. The present
CC sequence represents a specifically claimed soybean amino acid sequence
CC from the present invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from the USPTO web site.
XX
SQ Sequence 469 AA;

```
  Query Match             19.1%;  Score 78.5;  DB 11;  Length 469;
  Best Local Similarity   37.3%;  Pred. No. 0.78;
  Matches   25;  Conservative    8;  Mismatches   23;  Indels   11;  Gaps    5;

Qy         12 QMCVSSSSSSHDEAPVLNDK-HLDVPD---IIITPPTPTGMMLPRDLGSTVWLDETGSCP 67
              |  :    :||   |:|  | |||  :     :||||||  : | || ||  : :   |
Db         56 QNALHKLQNSH---PILRSKIHLDPSNNTFHFLTPPTPTVQIHPFDLASTAHIIQ---CQ 109

Qy         68 DDGEIDP 74
               ||  ||
Db        110 SDGH-DP 115
```

RESULT 10
AES72496
ID   AES72496 standard; peptide; 16 AA.
XX
AC   AES72496;
XX
DT   03-MAY-2007 (first entry)
XX
DE   Human C1958 protein mutant, amino acids 31-47.
XX
KW   Pancreatic ductal adenocarcinoma; cancer; cytostatic; tumor marker;
KW   protein therapy; screening; mutein; C1958V1; apoptosis; gene therapy;
KW   pancreas tumor; lung tumor; renal tumor; testicle tumor.
XX
OS   Homo sapiens.
OS   Synthetic.
OS   Unidentified.
XX
FH   Key   Location/Qualifiers
FT   Misc-difference 7. .11
FT   /note= "Wild-type Asp-Ile-Ile-ILe-Thr has been
FT   substituted by Val-Ile-Val-Ile-Thr"
XX
PN   WO2007013358-A2.
XX
PD   01-FEB-2007.
XX
PF   14-JUL-2006; 2006WO-JP314442.
XX
PR   28-JUL-2005; 2005US-0703791P.
XX
PA   (ONCO-) ONCOTHERAPY SCI INC.
PA   (UYTY) UNIV TOKYO.
XX
PI   Nakamura Y, Katagiri T, Inaki K;
XX

DR WPI; 2007-283242/27.
XX
PT New VIVIT polypeptide useful for treating or preventing cancer, such as
PT pancreatic cancer, lung cancer, kidney cancer and testicular tumor.
XX
PS Claim 3; SEQ ID NO 26; 78pp; English.
XX
CC The invention relates to a VIVIT polypeptide (AES72497) and at least a
CC fragment of the human C1958 sequence appearing as AES72472, in which
CC residues at positions 37-41 is replaced with AES72497, or an amino acid
CC sequence of a polypeptide functionally equivalent to the polypeptide
CC comprising the fragment sequence. Also included are an agent for
CC treating/preventing cancer (comprising as an active ingredient the VIVIT
CC polypeptide, or a polynucleotide encoding the polypeptide), a
CC pharmaceutical composition (comprising the VIVIT polypeptide, and a
CC carrier), screening (M1) for a compound useful in treating/preventing
CC cancers (involving (a) contacting a polypeptide comprising a PPP3CA-
CC binding domain of a C1958 polypeptide with a polypeptide comprising a
CC C1958-binding domain of a PPP3CA polypeptide in the presence of a test
CC compound, (b) detecting binding between the polypeptides, and (c)
CC selecting a test compound that inhibits binding between the
CC polypeptides), a kit for screening for a compound for treating or
CC preventing cancers, treating/preventing cancers in a subject (involving
CC administering the compound selected above), and inducing apoptosis in a
CC cell (involving introducing a polypeptide having a dominant-negative
CC effect against C1958 or a polynucleotide encoding the polypeptide into
CC the cell, where the polypeptide comprises a fragment sequence having
CC AES72497, or the mutated C1958 above). The polypeptide is modified with a
CC cell-membrane permeable substance, which has the general formula [R]-[D],
CC where [R] represents the cell-membrane permeable substance, and [D]
CC represents the amino acid sequence of a fragment sequence of AES72497, or
CC the mutated C1958 peptide. The VIVIT polypeptide is useful for treating
CC and/or preventing cancer, preferably pancreatic cancer (especially
CC Pancreatic ductal adenocarcinoma), lung cancer, kidney cancer and
CC testicular tumor. (M1) is useful for screening a compound for treating or
CC preventing cancers. The present sequence represents amino acids 31-47 of
CC human C1958V1, where the PPP3CA binding site at 37-41 has been replaced
CC by the VIVIT peptide.
XX
SQ Sequence 16 AA;

Query Match 19.0%; Score 78; DB 12; Length 16;
Best Local Similarity 87.5%; Pred. No. 0.013;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy         31 KHLDVPDIIITPPTPT 46
              |||||| |:|||||||
Db          1 KHLDVPVIVITPPTPT 16
```

RESULT 11
AES72479
ID AES72479 standard; peptide; 30 AA.
XX
AC AES72479;
XX
DT 03-MAY-2007 (first entry)
XX
DE C1958-PP3CA inhibitory peptide SEQ ID NO:9.
XX
KW Pancreatic ductal adenocarcinoma; cancer; cytostatic; tumor marker;
KW protein therapy; screening; apoptosis; gene therapy; pancreas tumor;
KW lung tumor; renal tumor; testicle tumor; C1958.
XX
OS Homo sapiens.
OS Synthetic.
OS Unidentified.
XX
PN WO2007013358-A2.
XX
PD 01-FEB-2007.
XX
PF 14-JUL-2006; 2006WO-JP314442.
XX
PR 28-JUL-2005; 2005US-0703791P.
XX
PA (ONCO-) ONCOTHERAPY SCI INC.
PA (UYTY) UNIV TOKYO.
XX
PI Nakamura Y, Katagiri T, Inaki K;
XX
DR WPI; 2007-283242/27.
XX
PT New VIVIT polypeptide useful for treating or preventing cancer, such as
PT pancreatic cancer, lung cancer, kidney cancer and testicular tumor.
XX
PS Example; SEQ ID NO 9; 78pp; English.
XX
CC The invention relates to a VIVIT polypeptide (AES72497) and at least a
CC fragment of the human C1958 sequence appearing as AES72472, in which
CC residues at positions 37-41 is replaced with AES72497, or an amino acid
CC sequence of a polypeptide functionally equivalent to the polypeptide
CC comprising the fragment sequence. Also included are an agent for
CC treating/preventing cancer (comprising as an active ingredient the VIVIT
CC polypeptide, or a polynucleotide encoding the polypeptide), a
CC pharmaceutical composition (comprising the VIVIT polypeptide, and a
CC carrier), screening (M1) for a compound useful in treating/preventing
CC cancers (involving (a) contacting a polypeptide comprising a PPP3CA-

CC binding domain of a C1958 polypeptide with a polypeptide comprising a
CC C1958-binding domain of a PPP3CA polypeptide in the presence of a test
CC compound, (b) detecting binding between the polypeptides, and (c)
CC selecting a test compound that inhibits binding between the
CC polypeptides), a kit for screening for a compound for treating or
CC preventing cancers, treating/preventing cancers in a subject (involving
CC administering the compound selected above), and inducing apoptosis in a
CC cell (involving introducing a polypeptide having a dominant-negative
CC effect against C1958 or a polynucleotide encoding the polypeptide into
CC the cell, where the polypeptide comprises a fragment sequence having
CC AES72497, or the mutated C1958 above). The polypeptide is modified with a
CC cell-membrane permeable substance, which has the general formula [R]-[D],
CC where [R] represents the cell-membrane permeable substance, and [D]
CC represents the amino acid sequence of a fragment sequence of AES72497, or
CC the mutated C1958 peptide. The VIVIT polypeptide is useful for treating
CC and/or preventing cancer, preferably pancreatic cancer (especially
CC Pancreatic ductal adenocarcinoma), lung cancer, kidney cancer and
CC testicular tumor. (M1) is useful for screening a compound for treating or
CC preventing cancers. The present sequence is a C1958 test peptide
CC comprising a polyArginine cell permeable peptide linked via a linker
CC peptide to a C1958 peptide where the residues corresponding to the PPP3CA
CC -binding site are replaced by a VIVIT peptide.
XX
SQ Sequence 30 AA;

Query Match 19.0%; Score 78; DB 12; Length 30;
Best Local Similarity 87.5%; Pred. No. 0.029;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy         31 KHLDVPDIIITPPTPT 46
              |||||| |:|||||||
Db         15 KHLDVPVIVITPPTPT 30
```

RESULT 12
AEJ38171
ID AEJ38171 standard; protein; 3792 AA.
XX
AC AEJ38171;
XX
DT 15-JUN-2007 (revised)
DT 21-SEP-2006 (first entry)
XX
DE P. cellulosum disC.
XX
KW Fungicide; disC; BOND_PC; DisC protein;
KW DisC protein [Polyangium cellulosum]; GO3824; GO8152; GO9058; GO16788;
KW GO16874; GO48037.
XX

OS Polyangium cellulosum.
XX
PN WO2006075013-A1.
XX
PD 20-JUL-2006.
XX
PF 12-JAN-2006; 2006WO-EP050169.
XX
PR 13-JAN-2005; 2005EP-00100190.
XX
PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
XX
PI Irschik H, Kopp M, Mueller R;
XX
DR WPI; 2006-549600/56.
DR N-PSDB; AEJ38168.
DR PC:NCBI; gi83698588.
XX
PT New proteins having the activity of translation products encoded by genes
PT disA, disE, disC, and disD obtainable from Sorangium cellulosum, useful
PT for producing polyketides, e.g. disorazole A1.
XX
PS Disclosure; SEQ ID NO 10; 41pp; English.
XX
CC The invention relates to proteins for the synthesis of a polyketide, the
CC proteins having the activity of translation products encoded by the genes
CC disA, disB, disC, and disD obtainable from Sorangium cellulosum in
CC combination with a translation product encoded by orf3-pTnRec_IE-2,
CC obtainable from S. cellulosum. The proteins, nucleic acids, and
CC microorganisms are useful for producing polyketides, e.g. disorazole A1.
CC The present sequence represents the amino acid sequence of P. cellulosum
CC disC.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 3792 AA;

Query Match 17.8%; Score 73; DB 11; Length 3792;
Best Local Similarity 28.2%; Pred. No. 54;
Matches 22; Conservative 12; Mismatches 30; Indels 14; Gaps 5;

```
Qy          4 KMSCLKGFQMCVSS------SSSSHDEAPVLNDKHLDVPDIIITPPT---PTGMMLPRD- 53
              ::   :| |:|:|:        : ||  |     ||    :| |  :   | | |:| |
Db       1098 RLPSFRGTQLCLSTERHLLDGEAEHDLGPTAGPDHLAY--VIYTSGSTGKPKGCMIPHDA 1155

Qy         54 -LGSTVWL-DETGSCPDD 69
                    :|: ||    |||
Db       1156 ICNRLLWMQDEYRLAPDD 1173
```

RESULT 13
AAO17533
ID AAO17533 standard; protein; 510 AA.
XX
AC AAO17533;
XX
DT 19-JUL-2002 (first entry)
XX
DE B glumae butinol I esterase.
XX
KW Esterase; enzyme; butinol I esterase; enantioselective ester hydrolysis;
KW organic ester interesterification.
XX
OS Burkholderia glumae.
XX
PN WO200218560-A2.
XX
PD 07-MAR-2002.
XX
PF 30-AUG-2001; 2001WO-EP010040.
XX
PR 31-AUG-2000; 2000DE-01042892.
PR 29-JUN-2001; 2001DE-01031544.
XX
PA (BADI) BASF AG.
XX
PI Hauer B, Friedrich T, Nuebling C, Stuermer R;
XX
DR WPI; 2002-393734/42.
DR N-PSDB; AAL46368.
XX
PT New butynol I esterase, for stereospecific hydrolysis or
PT transesterification of esters, to produce optically active reaction
PT products.
XX
PS Claim 2; Page 33-35; 36pp; German.
XX
CC The present invention provides the protein and coding sequences of
CC Burkholderia glumae (also known as Pseudomonas glumae) butinol I
CC esterase. The enzyme can be used for enantioselective ester hydrolysis
CC and transesterification reactions, to produce optically active alcohols,
CC carboxylic acids and esters. The present sequence is the protein of the
CC invention
XX
SQ Sequence 510 AA;

  Query Match   17.6%; Score 72.5; DB 5; Length 510;

```
  Best Local Similarity   23.7%;  Pred. No. 5.1;
  Matches   22;  Conservative   20;  Mismatches   22;  Indels   29;  Gaps    4;

Qy          2 GLKMSCLKGFQM-----------------CVSSSSSSHDEA---PVLND-------KHLD 34
              |:::| ::|  |                    ::::: || |   |  ::       :||
Db        279 GVELSAVEGGHMLPVTQPAATTDWLLAVAAAANAAAQHDAARPDPAPSEVTQAGALQHLK 338

Qy         35 VPDIIITPPTPTGMMLPRDL--GSTVWLDETGS 65
              | | ::    ||| ::  :|  | |:||  ||:
Db        339 VGDNVLIGKKPTGTLVADNLLPGKTLWLLSTGT 371
```

```
RESULT 14
AFP89144
ID   AFP89144 standard; protein; 96 AA.
XX
AC   AFP89144;
XX
DT   18-OCT-2007  (first entry)
XX
DE   Glycine max protein SEQ ID NO:180322.
XX
KW   plant; cold tolerance; heat tolerance; drought resistance;
KW   herbicide resistance; pathogen resistance; pesticide resistance;
KW   disease-resistance; crop improvement; insect resistance;
KW   nitrogen fixation; plant growth regulation; plant disease;
KW   stress tolerance; seed oil; transgenic.
XX
OS   Glycine max.
XX
PN   US2004031072-A1.
XX
PD   12-FEB-2004.
XX
PF   28-APR-2003; 2003US-00424599.
XX
PR   06-MAY-1999;   99US-00304517.
PR   05-NOV-2001; 2001US-00985678.
XX
PA   (LROS/) LA ROSA T J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (CAOY/) CAO Y.
XX
PI   La Rosa TJ,  Zhou Y,  Kovalic DK,  Cao Y;
XX
DR   WPI; 2004-168999/16.
XX
PT   New recombinant DNA construct, useful in producing plants with desired
```

PT properties, e.g. increased cold, heat or drought tolerance or tolerance
PT to herbicides, extreme osmotic conditions or pathogens and improved plant
PT growth and development.
XX
PS Claim 2; SEQ ID NO 180322; 15pp; English.
XX
CC The invention relates to a recombinant DNA construct, polynucleotides or
CC polypeptides which are useful in improving plant cold, heat or drought
CC tolerance or tolerance to herbicides, extreme osmotic conditions,
CC pathogens or pests, in improving yield by modification of photosynthesis
CC or of carbohydrate, nitrogen or phosphorus use and/or uptake, in
CC manipulating growth rate in plant cells by modification of the cell cycle
CC pathway, in providing increased resistance to plant disease and improved
CC plant growth and development under at least one stress condition, in
CC producing galactomannan, plant growth regulators and lignin, in
CC increasing the rate of homologous recombination in plants, in modifying
CC seed oil yield and/or content and seed protein yield and/or content and
CC in encoding a plant transcription factor. The present sequence represents
CC a Glycine max protein of the invention. Note: This sequence is not shown
CC in the specification but was obtained in electronic format directly from
CC USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 96 AA;

Query Match 17.5%; Score 72; DB 8; Length 96;
Best Local Similarity 31.2%; Pred. No. 0.74;
Matches 20; Conservative 5; Mismatches 23; Indels 16; Gaps 2;

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Qy         10 GFQMCVSSSSSSHDEAPVLNDKHLDVPDIIITPPTPTGMMLPRDLGSTVWLDETGSCPDD 69
              | | | |:| |:|  :|         | :   |||        ||| | |   |    |
Db         13 GEQFCSSASCSTHHHSP---------PSLPFRPPT-------GDLGQTEWTASTLKHIDS 56

Qy         70 GEID 73
               : |
Db         57 SDYD 60
```

RESULT 15
ABU18188
ID ABU18188 standard; protein; 1302 AA.
XX
AC ABU18188;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #3715.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX

OS Bacillus anthracis.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA22058.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 46112; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the

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CC   proliferation of an organism. The antisense nucleic acids are useful for
CC   identifying proteins or screening for homologous nucleic acids required
CC   for cellular proliferation to isolate candidate molecules for rational
CC   drug discovery programs, or for screening homologous nucleic acids
CC   required for proliferation in cells other than S. aureus, S. typhimurium,
CC   K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC   the target prokaryotic essential genes. Note: The sequence data for this
CC   patent did not form part of the printed specification, but was obtained
CC   in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1302 AA;

  Query Match             17.2%;  Score 70.5;  DB 6;  Length 1302;
  Best Local Similarity   34.0%;  Pred. No. 30;
  Matches   18;  Conservative   13;  Mismatches   15;  Indels    7;  Gaps    2;

Qy         17 SSSSSHDEAPVLNDKHLDVPDIIITPPT-----PTGMMLPRD--LGSTVWLDE 62
              ||:   ::| |:| :  || ::: ||||      | : :|:   | :| ||:|
Db        811 SSTEVEEKAYVVNQRENDVRNVLQTPPTYTIPSLTLLSIPQQAALDNTEWLEE 863


Search completed: April 10, 2008, 01:18:54
Job time : 312.833 secs
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